

09424347 Results

SEQ ID NO: 2

SUMMARIES

Result	No.	Score	Query Match	Length	DB	ID	Description
	1	2924	100.0	563	20	AAW88489	Human organic anio
	2	2832.5	96.9	550	21	AAV44278	Human organic anio
	3	2832.5	96.9	550	22	AAB47271	hOAT1. Homo sapie
	4	2532	86.6	551	20	AAW88488	Rat organic anion
	5	2457	84.0	545	22	AAB36553	Mouse organic anio
	6	1410.5	48.2	542	22	AAB47274	hOAT3. Homo sapie
	7	1409.5	48.2	542	21	AAV92902	Human cerebral org
	8	1369	46.8	561	18	AAW44196	Human osteoclast t
	9	1368.5	46.8	537	18	AAW44195	Mouse osteoclast t
	10	1366.5	46.7	536	21	AAV92903	Rat cerebral organ
	11	1225.5	41.9	553	22	AAE10332	Human transporter
	12	1206	41.2	578	22	AAE06571	Human protein havi
	13	1206	41.2	815	22	ABG26899	Novel human diagno
	14	1127	38.5	550	22	AAE06612	Human protein havi
	15	1127	38.5	550	22	AAB69091	Human organic anio
	16	1115	38.1	566	22	AAE10336	Human transporter
	17	1058.5	36.2	541	22	AAB47276	hOAT5. Homo sapie
	18	996	34.1	535	21	AAV51249	Rat liver anion tr

RESULT 1

AAW88489

ID AAW88489 standard; Protein; 563 AA.

XX

AC AAW88489;

XX

DT 05-MAR-1999 (first entry)

XX

DE Human organic anion transporter OAT-1.

XX

KW Organic anion transporter; OAT-1; nephrotoxicity; drug release;

KW drug-drug interaction mechanism; drug elimination; kidney;

KW beta-lactam antibiotic; non-steroidal antiinflammatory; diuretic.

XX

OS Homo sapiens.

XX

PN W09853064-A1.

XX

PD 26-NOV-1998.

XX

PF 18-MAY-1998; 98WO-JP02171.

XX

PR 23-MAY-1997; 97JP-0134182.

XX

PA (TANA) TANABE SEIYAKU CO.

XX

PI Endou H, Hosoyamada M, Kanai Y, Sekine T;

XX

DR WPI; 1999-045310/04.

DR

N-PSDB; AAV79585.

XX

PT New renal organic anion transporter protein - useful for, e.g.

PT screening potential drugs for prevention of nephrotoxicity and as a

PT reagent for the investigation of drug metabolism

XX

PS Claim 1; Page 27-32; 45pp; Japanese.

XX

CC The present sequence represents human organic anion transporter protein

CC OAT-1. OAT-1 may be used as a reagent for the in vitro analysis and

CC study of drug release and drug-drug interaction mechanisms and drug

CC elimination via the kidney (e.g. for drugs such as beta-lactam

CC antibiotics, non-steroidal antiinflammatories and diuretics), and as

CC a reagent for screening candidate drugs for the prevention of
CC nephrotoxicity. Oligonucleotide sequences which hybridise to the OAT-1
CC polynucleotide may be used as probes for detection of OAT-1 gene
CC sequences.

XX

SQ Sequence 563 AA;

Query Match 100.0%; Score 2924; DB 20; Length 563;
Best Local Similarity 100.0%; Pred. No. 7.2e-290;
Matches 563; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 MAFNDLLQQVGGVGRFQQIQVTLVVLPPLLMAHNTLQNFTAAIPTHHCRPPADANLSKN 60
      |||
Db      1 mafndllqqvggvgvgrfqqiqvtlvvlplllmashntlnftaaipthhcrppadanlskn 60

Qy     61 GGLEVLVPRDRQGQPESCLRFTSPQWGLPFLNGTEANGTGATEPCTDGWIYDNSTFPSTI 120
      |||
Db     61 gglevvlprdrqgqpescrlftspqwgplflngteangtgatepctdgwydnstfpsti 120

Qy    121 VTEWDLVCSHRALRQLAQSLYMGVLLGAMVFGYLADRLGRRKVLILNYLQTAVSGTCAA 180
      |||
Db    121 vtewdlvcshralrqlaqslymgvllgamvfgyladrlgrrkvililnylqtavsgtcaa 180

Qy    181 FAPNFPYICAFRLSGMALAGISLNCMTLNVWEMPIHTRACVGTIGYVYSLGQFLLAGV 240
      |||
Db    181 fapnfpicycafrllsgmalagislncmtlnvewmpihtracvgtligvyvslgqfllagv 240

Qy    241 AYAVPHWRHLQLLVSAPFFAFFIYSWFFIESARWHSSSGRLDRTLALQRVARINGKREE 300
      |||
Db    241 ayavphwrhlqllvsapffaffiyswffiesarwhsssgrldrtlalqrvaringkree 300

Qy    301 GAKLSMEVLRASLQKELTMGKGQASAMELLRCPTLRHLFLCLSMWLFATSFAYYGLVMDL 360
      |||
Db    301 gaklsmevlraslqkeltmgkgqasamellrcptlrhlflclsmwlfatsfayyglvmdl 360

Qy    361 QGFGVSIYLIQVIFGAVDLPKLVGFLVINSIGRRPAQMAALLLAGICILNGVIPQDQS 420
      |||
Db    361 qgfgvsiyliqvifgavdlpaklvgflvinslgrrpaqmaalllagicilngvipqdds 420

Qy    421 IVRTSLAVLGKGLAASFNCIFLYTGELYPTMIRQTGMGMGSTMARVGSIVSPLVSMTAE 480
      |||
Db    421 ivrtslavlgkgclaasfnciflytgelyptmirqrgmngstmarvgsivsplvsmtae 480

Qy    481 LYPSPMLFIYGAVPVAASAVTVLLPETLGQPLPDTVQDLESRWAPTQKEAGIYPRKGKQT 540
      |||
Db    481 lypsplmfiygapvvaasavtvllpetlgqplpdtvqdlesrwaptqkeagiypkkgkqt 540

Qy    541 RQQQEHQKYMVPLQASAEKNGL 563
      |||
Db    541 rqqqehqkymvplqasaeekngl 563
```

RESULT 4

AAW88488

ID AAW88488 standard; Protein; 551 AA.

XX

AC AAW88488;

XX

DT 05-MAR-1999 (first entry)

XX

DE Rat organic anion transporter OAT-1.

XX

KW Organic anion transporter; OAT-1; nephrotoxicity; drug release;

KW drug-drug interaction mechanism; drug elimination; kidney;

KW beta-lactam antibiotic; non-steroidal antiinflammatory; diuretic.

XX

OS Rattus sp.

XX

PN W09853064-A1.

```

XX
PD 26-NOV-1998.
XX
PF 18-MAY-1998; 98WO-JP02171.
XX
PR 23-MAY-1997; 97JP-0134182.
XX
PA (TANA ) TANABE SEIYAKU CO.
XX
PI Endou H, Hosoyamada M, Kanai Y, Sekine T;
XX
DR WPI; 1999-045310/04.
DR N-PSDB; AAV79584.
XX
PT New renal organic anion transporter protein - useful for, e.g.
PT screening potential drugs for prevention of nephrotoxicity and as a
PT reagent for the investigation of drug metabolism
XX
PS Claim 1; Page 22-26; 45pp; Japanese.
XX
CC The present sequence represents rat organic anion transporter protein
CC OAT-1. OAT-1 may be used as a reagent for the in vitro analysis and
CC study of drug release and drug-drug interaction mechanisms and drug
CC elimination via the kidney (e.g. for drugs such as beta-lactam
CC antibiotics, non-steroidal antiinflammatories and diuretics), and as
CC a reagent for screening candidate drugs for the prevention of
CC nephrotoxicity. Oligonucleotide sequences which hybridise to the OAT-1
CC polynucleotide may be used as probes for detection of OAT-1 gene
CC sequences.
XX
SO Sequence 551 AA;

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```

Db      481 fypsmplfifgavpvvasavtallpetlgqplpdtvqdlksr-----srgkqn 528
Qy      541 RQQQEHQKYMVPLQASAEKNGL 563
      :|||| | | :|||| | |||||
Db      529 qqqqeqqkqmmplqastqekngl 551

```


Result		Query				ID	Description
No.	Score	Match	Length	DB			
1	628	21.5	557	1	OCN2_HUMAN	O76082	homo sapien
2	626	21.4	557	1	OCN2_MOUSE	Q9z0e8	mus musculu
3	626	21.4	557	1	OCN2_RAT	O70594	rattus norv
4	387	13.2	529	1	YOU1_CAEEL	P30638	caenorhabdi
5	334	11.4	751	1	YLX5_CAEEL	P46501	caenorhabdi
6	275	9.4	435	1	YT13_CAEEL	Q10917	caenorhabdi
7	261	8.9	400	1	YCEI_BACSU	O34691	bacillus su
8	260.5	8.9	482	1	YFIG_BACSU	P54723	bacillus su
9	240.5	8.2	445	1	YGCS_ECOLI	Q46909	escherichia
10	239.5	8.2	742	1	SYV2_RAT	Q02563	rattus norv
11	239	8.2	1222	1	YMP3_CAEEL	Q10947	caenorhabdi
12	229	7.8	451	1	YYAJ_BACSU	P37514	bacillus su

RESULT 4

YOU1_CAEEL

ID YOU1_CAEEL STANDARD; PRT; 529 AA.

AC P30638; Q21101;

DT 01-APR-1993 (Rel. 25, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 01-MAR-2002 (Rel. 41, Last annotation update)

DE Hypothetical 58.3 kDa protein ZK637.1 in chromosome III.

GN ZK637.1.

OS Caenorhabditis elegans.

OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;

OC Rhabditidae; Peloderinae; Caenorhabditis.

OX NCBI_TaxID=6239;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=BRISTOL N2;

RX MEDLINE=92168156; PubMed=1538779;

RA Sulston J., Du Z., Thomas K., Wilson R., Hillier L., Staden R.,

RA Halloran N., Green P., Thierry-Mieg J., Qiu L., Dear S., Coulson A.,

RA Craxton M., Durbin R.K., Berks M., Metzstein M., Hawkins T.,

RA Ainscough R., Waterston R.;

RT "The C. elegans genome sequencing project: a beginning.";

RL Nature 356:37-41(1992).

RN [2]

RP REVISIONS.

RC STRAIN=BRISTOL N2;

RA Durbin R.;

RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.

CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Probable).

CC -!- SIMILARITY: BELONGS TO THE SUGAR TRANSPORTER FAMILY.

 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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 CC or send an email to license@isb-sib.ch).
 CC -----

DR EMBL; Z11115; CAA77460.1; -.

DR EMBL; Z22175; CAA77460.1; JOINED.

DR EMBL; Z22175; CAA80131.1; -.

DR EMBL; Z11115; CAA80131.1; JOINED.

DR PIR; S15786; S15786.

DR WormPep; ZK637.1; CE06638.

DR InterPro; IPR003662; sub_transporter.

DR Pfam; PF00083; sugar_tr; 1.

DR PROSITE; PS00216; SUGAR_TRANSPORT_1; FALSE_NEG.

DR PROSITE; PS00217; SUGAR_TRANSPORT_2; FALSE_NEG.

KW Hypothetical protein; Transmembrane; Transport.

FT DOMAIN 1 85 CYTOPLASMIC (POTENTIAL).

FT	TRANSMEM	86	106	1 (POTENTIAL).
FT	DOMAIN	107	120	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	121	141	2 (POTENTIAL).
FT	DOMAIN	142	157	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	158	178	3 (POTENTIAL).
FT	DOMAIN	179	179	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	180	200	4 (POTENTIAL).
FT	DOMAIN	201	208	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	209	229	5 (POTENTIAL).
FT	DOMAIN	230	237	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	238	258	6 (POTENTIAL).
FT	DOMAIN	259	319	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	320	340	7 (POTENTIAL).
FT	DOMAIN	341	372	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	373	393	8 (POTENTIAL).
FT	DOMAIN	394	410	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	411	431	9 (POTENTIAL).
FT	DOMAIN	432	434	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	435	455	10 (POTENTIAL).
FT	DOMAIN	456	461	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	462	480	11 (POTENTIAL).
FT	DOMAIN	481	482	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	483	502	12 (POTENTIAL).
FT	DOMAIN	503	529	CYTOPLASMIC (POTENTIAL).
SQ	SEQUENCE	529 AA;	58317 MW;	8D2FF4CBA15ECD2D CRC64;

Query Match 13.2%; Score 387; DB 1; Length 529;
 Best Local Similarity 25.9%; Pred. No. 5.6e-22;
 Matches 128; Conservative 80; Mismatches 205; Indels 82; Gaps 15;

Qy	64	EVWLPDRDQGPESCLRFTSPQWGLPFLNGTEANGTGATEPCTD-----GWIYDN-----	113
Db	51	ELGEPTD-QRSPDSEKTFTVDE-----AVEALGFRFQLKLSILTGMAMMADAMEMML	102
Qy	114	-STFPSTIVTEWDLVCSHRALRQLAQSLYMGVLLGAMVFGYLADRLGRRKVLILNYLQT	172
Db	103	LSLISPALACEWGISSVQQA---LVTTCVFSGMMLSSTFWGKICDRFRRKGLTFSTLVA	159
Qy	173	AVSGTCAAFAPNFPIYCAFRLLSGMALAGISLNCMTLNVEWMPHTRACVGTIGYVYSL	232
Db	160	CIMGVISGMSPHFYVLLFFRGLTGFGIGGVP-QSVTLYAEFLPTAQRAKCVVLIESFWAI	218
Qy	233	GQFLLAGVAYAVPH---WRHLQLLVSAFFFAFFIYSWFFIESARWHSSSGRLDLTLRALQ	289
Db	219	GAVFEALLAYFVMESFGWRALMFLSSLPGLIFAVASFWLPESARFDMASGHPERALETQ	278
Qy	290	RVARINGKREEGAKLSMEVLRASLQKELTMGKGQASAMELLRCPTLRHLFLCLSMWFAT	349
Db	279	AAARMN-----RVQLPTGRLVSSTKAGSESRGDIANLLSPDLRKTILLWCWAIT	329
Qy	350	SFAYYGLVM-----DLQFGVSIYLIQVIFGA-----VDLPAKLVG	385
Db	330	AFSYYGMVLFSTTVLQSHDECHGGLFSNGTQMEVCQPLTRSDYFDLLSTTLAEFGLIIT	389
Qy	386	FLVINSIGRRPAQMAALLLAGI-----CILLNGVIPQDQSIVRTSLAVLGKGCLAASF	438
Db	390	VLIIEWFGRKKTMALEYAVFAIFTFLLYFCL-----DRFTV-TVLIFVARAFISGAF	440
Qy	439	NCIFLYTGELYPTMIRQTGMGMGSTMARVGSIVSPLVSMATAELYSMPFLFIYGAVPVAAS	498
Db	441	QCAYVYTPEVYPTTLRAVGLGTCSAMARIGAIVASEKSL-----SLPIGIYGTAAILGL	494
Qy	499	AVTVLLP-ETLGQPL	512
Db	495	IASLSLPIETKGRQM	509

SUMMARIES

Result	%	Query
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No.	Score	Match	Length	DB	ID	Description
1	2924	100.0	563	4	O95742	O95742 homo sapien
2	2675	91.5	519	4	Q9NQA6	Q9nqa6 homo sapien
3	2583.5	88.4	506	4	Q9NQC2	Q9nqc2 homo sapien
4	2571	87.9	551	6	Q9TSY7	Q9tsy7 oryctolagus
5	2543	87.0	551	11	O35956	O35956 rattus norv
6	2443	83.5	545	11	Q61185	Q61185 mus musculu
7	1411.5	48.3	562	13	O57379	O57379 pseudopleur
8	1409.5	48.2	542	4	Q96TC1	Q96tc1 homo sapien
9	1376.5	47.1	537	11	O88909	O88909 mus musculu
10	1376.5	47.1	537	11	Q91WJ9	Q91wj9 mus musculu
11	1366.5	46.7	536	11	Q9R1U7	Q9rlu7 rattus norv
12	1267.5	43.3	553	11	O54778	O54778 mus musculu
13	1225.5	41.9	553	4	Q96S37	Q96s37 homo sapien
14	1204.5	41.2	568	4	O95820	O95820 homo sapien
15	1127	38.5	550	4	Q9NSA0	Q9nsa0 homo sapien

RESULT 1

O95742

ID O95742 PRELIMINARY; PRT; 563 AA.

AC O95742; O95187; Q9UEQ8; Q9UBG6;

DT 01-MAY-1999 (TrEMBLrel. 10, Created)

DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)

DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)

DE RENAL ORGANIC ANION TRANSPORT PROTEIN 1.

GN SLC22A6 OR OAT1 OR ROAT1.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A., AND CHARACTERIZATION.

RC TISSUE=KIDNEY;

RX MEDLINE=99103997; PubMed=9887087;

RA Hosoyamada M., Sekine T., Kanai Y., Endou H.;

RT "Molecular cloning and functional expression of a multispecific

RT organic anion transporter from human kidney.";

RL Am. J. Physiol. 276:F122-F128(1999).

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=98433806; PubMed=9762842;

RA Reid G., Wolff N.A., Dautzenberg F.M., Burckhardt G.;

RT "Cloning of a human renal p-aminohippurate transporter, hROAT1.";

RL Kidney Blood Press. Res. 21:233-237(1998).

RN [3]

RP SEQUENCE FROM N.A.

RC TISSUE=KIDNEY;

RX MEDLINE=99137667; PubMed=9950961;

RA Lu R., Chan B.S., Schuster V.L.;

RT "Cloning of the human kidney PAH transporter: narrow substrate

RT specificity and regulation by protein kinase C.";

RL Am. J. Physiol. 276:F295-F303(1999).

RN [4]

RP SEQUENCE FROM N.A.

RC TISSUE=KIDNEY;

RX MEDLINE=99160894; PubMed=10049739;

RA Race J.E., Grassl S.M., Williams W.J., Holtzman E.J.;

RT "Molecular cloning and characterization of two novel human renal

RT organic anion transporters (hOAT1 and hOAT3).";

RL Biochem. Biophys. Res. Commun. 255:508-514(1999).

RN [5]

RP SEQUENCE FROM N.A.

RC TISSUE=KIDNEY;

RX MEDLINE=99393620; PubMed=10462545;

RA Cihlar T., Lin D.C., Pritchard J.B., Fuller M.D., Mendel D.B.,

RT Sweet D.H.;

RT "The antiviral nucleotide analogs cidofovir and adefovir are novel

RT substrates for human and rat renal organic anion transporter 1.";

RL Mol. Pharmacol. 56:570-580(1999).
 RN [6]
 RP SEQUENCE FROM N.A.
 RA Bahn A., Prawitt D., Reid G., Enklaar T., Wolff N.A., Hillemann A.,
 RA Godehardt S., Buttler D., Knabe M., Schulten H.J., Gunawan B.,
 RA Fuezesi L., Zabel B., Burckhardt G.;
 RT "Genomic cloning and characterization of the human renal organic anion
 RT transporter gene (hOAT1).";
 RL Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
 CC -!- FUNCTION: MEDIATES THE NA(+)-INDEPENDENT TRANSPORT OF ORGANIC
 CC ANIONS SUCH AS P-AMINOHIPPURATE AND ALPHA-KETOGLUTARATE.
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. BASOLATERAL
 CC MEMBRANE (POTENTIAL).
 CC -!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; ISOFORM HOAT1-1 (SHOWN HERE)
 CC AND ISOFORM HOAT1-2; ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -!- TISSUE SPECIFICITY: STRONGLY EXPRESSED IN KIDNEY. ALSO DETECTED IN
 CC BRAIN AND AT LOW LEVELS, IN SKELETAL MUSCLE AND PLACENTA. NOT
 CC EXPRESSED IN HEART, LUNG, LIVER, PANCREAS, COLON, THYMUS, SMALL
 CC INTESTINE OR PERIPHERAL BLOOD LEUKOCYTES. IN THE KIDNEY, STRONGLY
 CC EXPRESSED IN PROXIMAL TUBULE CELLS.
 CC -!- PTM: GLYCOSYLATED.
 CC -!- SIMILARITY: BELONGS TO THE SLC22 FAMILY OF TRANSPORTERS.
 DR EMBL; AF057039; AAC70004.1; -.
 DR EMBL; AB009697; BAA75072.1; -.
 DR EMBL; AF104038; AAD10052.1; -.
 DR EMBL; AB009698; BAA75073.1; -.
 DR EMBL; AF097490; AAD19356.1; -.
 DR EMBL; AF124373; AAD55356.1; -.
 DR EMBL; AJ249369; CAB77184.1; -.
 DR InterPro; IPR003662; sub_transporter.
 DR Pfam; PF00083; sugar_tr; 1.
 KW Transmembrane; Transport; Alternative splicing; Ion transport;
 KW Glycoprotein.
 FT TRANSMEM 136 156 POTENTIAL.
 FT TRANSMEM 185 205 POTENTIAL.
 FT TRANSMEM 249 269 POTENTIAL.
 FT TRANSMEM 338 358 POTENTIAL.
 FT TRANSMEM 396 416 POTENTIAL.
 FT TRANSMEM 426 446 POTENTIAL.
 FT TRANSMEM 485 505 POTENTIAL.
 FT CARBOHYD 39 39 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 56 56 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 92 92 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 97 97 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 113 113 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT VARSPLIC 523 535 MISSING (IN ISOFORM OAT1.2).
 FT CONFLICT 14 14 G -> S (IN REF. 3).
 FT CONFLICT 563 563 L -> F (IN REF. 2).
 SQ SEQUENCE 563 AA; 61816 MW; 74AD3EA2678032E4 CRC64;

Query Match 100.0%; Score 2924; DB 4; Length 563;
 Best Local Similarity 100.0%; Pred. No. 1.9e-227;
 Matches 563; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MAFNDDLQQVGGRFQQIQVTLVVLP LLLMASHNTLQNFTAAIPTHHCRPPADANLSKN	60
Db	1	MAFNDDLQQVGGRFQQIQVTLVVLP LLLMASHNTLQNFTAAIPTHHCRPPADANLSKN	60
Qy	61	GGLEVWLPDRDQQPESCLRFTSPQWGLPFLNGTEANGTGATEPCTDGGWIYDNSTFPSTI	120
Db	61	GGLEVWLPDRDQQPESCLRFTSPQWGLPFLNGTEANGTGATEPCTDGGWIYDNSTFPSTI	120
Qy	121	VTEWDLVCSHRALRQLAQSLYMGVLLGAMVFGYLADRLGRRKVLILNYLQTAVSGTCAA	180
Db	121	VTEWDLVCSHRALRQLAQSLYMGVLLGAMVFGYLADRLGRRKVLILNYLQTAVSGTCAA	180
Qy	181	FAPNFPPIYCAFRLLSGMALAGISLNCMTLNVEWMPHTRACVGTIGYVYSLGQFLLAGV	240
Db	181	FAPNFPPIYCAFRLLSGMALAGISLNCMTLNVEWMPHTRACVGTIGYVYSLGQFLLAGV	240

Qy 241 AYAVPHWRHLQLLVSAFFFAFFIYSWFFIESARWHSSSGRLDLTLRALQRVARINGKREE 300
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 241 AYAVPHWRHLQLLVSAFFFAFFIYSWFFIESARWHSSSGRLDLTLRALQRVARINGKREE 300
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Qy 301 GAKLSMEVLRASLQKELTMGKGQASAMELLRCPTLRHLFLCLSMWLFATSFAYYGLVMDL 360
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 301 GAKLSMEVLRASLQKELTMGKGQASAMELLRCPTLRHLFLCLSMWLFATSFAYYGLVMDL 360
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Qy 361 QGFGVSIYLIQVIFGAVDLPAKLVGFLVINSIGRRPAQMAALLLAGICILLNGVIPQDQS 420
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 361 QGFGVSIYLIQVIFGAVDLPAKLVGFLVINSIGRRPAQMAALLLAGICILLNGVIPQDQS 420
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Qy 421 IVRTSLAVLGKGLAASFNCIFLYTGELYPTMIRQTGMGMGSTMARVGSIVSPLVSMTAE 480
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 421 IVRTSLAVLGKGLAASFNCIFLYTGELYPTMIRQTGMGMGSTMARVGSIVSPLVSMTAE 480
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Qy 481 LYPSPMLFIYGAVPVAASAVTVLLPETLGQPLPDTVQDLESRWAPTQKEAGIYPRKGKQT 540
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 481 LYPSPMLFIYGAVPVAASAVTVLLPETLGQPLPDTVQDLESRWAPTQKEAGIYPRKGKQT 540
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Qy 541 RQQQEHQKYMVPLQASAEKNGL 563
 ||||||||||||||||||||
 Db 541 RQQQEHQKYMVPLQASAEKNGL 563
 ||||||||||||||||||||

RESULT 5

O35956

ID O35956 PRELIMINARY; PRT; 551 AA.
 AC O35956;
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE RENAL ORGANIC ANION TRANSPORT PROTEIN 1.
 GN SLC22A6 OR ROAT1.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A., FUNCTION, AND TISSUE SPECIFICITY.
 RC TISSUE=KIDNEY;
 RX MEDLINE=98043701; PubMed=9374486;
 RA Sweet D.H., Wolff N.A., Pritchard J.B.;
 RT "Expression cloning and characterization of ROAT1. The basolateral
 RT organic anion transporter in rat kidney.";
 RL J. Biol. Chem. 272:30088-30095(1997).
 RN [2]
 RP SEQUENCE FROM N.A., FUNCTION, AND TISSUE SPECIFICITY.
 RC STRAIN=SPRAGUE-DAWLEY; TISSUE=KIDNEY;
 RX MEDLINE=97373539; PubMed=9228014;
 RA Sekine T., Watanabe N., Hosoyamada M., Kanai Y., Endou H.;
 RT "Expression cloning and characterization of a novel multispecific
 RT organic anion transporter.";
 RL J. Biol. Chem. 272:18526-18529(1997).
 CC -!- FUNCTION: MEDIATES THE NA(+)-INDEPENDENT TRANSPORT OF ORGANIC
 CC ANIONS SUCH AS CYCLIC NUCLEOTIDES, PROSTAGLANDIN E2 AND URIC ACID.
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. BASOLATERAL
 CC MEMBRANE (POTENTIAL).
 CC -!- TISSUE SPECIFICITY: STRONG EXPRESSION IN KIDNEY. VERY WEAK
 CC EXPRESSION IN BRAIN. NOT DETECTED IN HEART, LUNG, LIVER, SPLEEN
 CC SKELETAL MUSCLE, SMALL INTESTINE, LARGE INTESTINE, EYE OR TESTIS.
 CC EXPRESSED IN THE PROXIMAL TUBULE IN THE KIDNEY.
 CC -!- PTM: GLYCOSYLATED (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO THE SLC22 FAMILY OF TRANSPORTERS.
 DR EMBL; AF008221; AAC18772.1; -.
 DR EMBL; AB004559; BAA22086.1; -.
 DR InterPro; IPR003662; sub_transporter.
 DR Pfam; PF00083; sugar_tr; 1.
 KW Transmembrane; Transport; Glycoprotein; Ion transport.
 FT TRANSMEM 136 156 POTENTIAL.

FT	TRANSMEM	196	216	POTENTIAL.
FT	TRANSMEM	249	269	POTENTIAL.
FT	TRANSMEM	338	358	POTENTIAL.
FT	TRANSMEM	396	416	POTENTIAL.
FT	TRANSMEM	485	505	POTENTIAL.
FT	CARBOHYD	39	39	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	56	56	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	92	92	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	97	97	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	113	113	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	184	184	N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ	SEQUENCE	551 AA;	60766 MW;	8BA47BE628324BF2 CRC64;

Query Match 87.0%; Score 2543; DB 11; Length 551;
 Best Local Similarity 86.0%; Pred. No. 9.5e-197;
 Matches 484; Conservative 35; Mismatches 32; Indels 12; Gaps 1;

Qy	1	MAFN	DL	LQ	QV	GG	VG	RF	Q	Q	I	Q	V	T	L	V	V	L	P	L	L	M	A	S	H	N	T	L	Q	N	F	T	A	A	I	P	T	H	C	R	P	P	A	D	A	N	L	S	K	N	60								
Db	1	MAFN	DL	LQ	QV	GG	VG	RF	Q	Q	I	Q	V	T	L	V	V	L	P	L	L	M	A	S	H	N	T	L	Q	N	F	T	A	A	I	P	P	H	C	R	P	P	A	N	L	S	K	D	60										
Qy	61	GGLE	VW	LP	RD	RQ	GP	ES	CL	RF	TSP	QW	GL	P	FL	NG	TE	AN	GT	GA	TE	P	C	T	D	G	W	I	D	N	S	T	F	P	S	T	I	120																					
Db	61	GGLE	AW	LP	LD	KQ	GP	ES	CL	RF	TSP	QW	GP	P	F	Y	NG	TE	AN	GT	RV	TE	P	C	I	D	G	W	V	D	N	S	T	F	P	S	T	I	120																				
Qy	121	VTEW	DL	VC	SH	RA	L	R	Q	L	A	Q	S	L	Y	M	V	G	V	L	G	A	M	V	F	G	Y	L	A	D	R	L	G	R	R	K	V	L	I	N	Y	L	Q	T	A	V	S	G	T	C	A	180							
Db	121	VTEW	N	L	VC	SH	R	A	F	R	Q	L	A	Q	S	L	Y	M	V	G	V	L	G	A	M	V	F	G	Y	L	A	D	R	L	G	R	R	K	V	L	I	N	Y	L	Q	T	A	V	S	G	T	C	A	180					
Qy	181	FAPN	F	P	I	Y	C	A	F	R	L	S	G	M	A	L	A	G	I	S	L	N	C	M	T	L	N	V	E	W	M	P	I	H	T	R	A	C	V	G	T	L	I	G	Y	V	Y	S	L	G	F	L	L	A	G	V	240		
Db	181	YAPN	Y	T	V	Y	C	V	F	R	L	S	G	M	S	L	A	I	A	I	N	C	M	T	L	N	V	E	W	M	P	I	H	T	R	A	V	G	T	L	I	G	Y	V	Y	S	L	G	F	L	L	A	G	I	240				
Qy	241	AYAV	P	H	R	H	L	Q	L	L	V	S	A	P	F	F	A	F	I	Y	S	W	F	F	I	E	S	A	R	W	H	S	S	S	G	R	L	D	L	T	L	R	A	L	Q	R	V	A	R	I	N	G	K	R	E	300			
Db	241	AYAV	P	H	R	H	L	Q	L	V	S	V	P	F	F	I	A	F	I	Y	S	W	F	F	I	E	S	A	R	W	Y	S	S	S	G	R	L	D	L	T	L	R	A	L	Q	R	V	A	R	I	N	G	K	Q	E	300			
Qy	301	GAKL	S	M	E	V	L	R	A	S	L	Q	K	E	L	T	M	G	K	G	Q	A	S	A	M	E	L	L	R	C	P	T	L	R	H	L	F	L	C	S	M	L	W	F	A	T	S	F	A	Y	Y	G	L	V	M	D	L	360	
Db	301	GAKL	S	I	E	V	L	R	T	S	L	Q	K	E	L	T	L	S	K	G	Q	A	S	A	M	E	L	L	R	C	P	T	L	R	H	L	F	L	C	S	M	L	W	F	A	T	S	F	A	Y	Y	G	L	V	M	D	L	360	
Qy	361	QGFG	V	S	I	Y	L	I	Q	V	I	F	G	A	V	D	L	P	A	K	L	V	G	F	L	V	I	N	S	L	G	R	R	P	A	Q	M	A	L	L	L	A	G	I	C	I	L	N	G	V	I	P	Q	D	S	420			
Db	361	QGFG	V	S	M	Y	L	I	Q	V	I	F	G	A	V	D	L	P	A	K	F	V	C	F	L	V	I	N	S	M	G	R	R	P	A	Q	M	A	S	L	L	L	A	G	I	C	I	L	N	G	I	P	K	S	H	T	420		
Qy	421	IVRT	S	L	A	V	L	G	K	G	C	L	A	A	S	F	N	C	I	F	L	Y	T	G	E	L	Y	P	T	M	I	R	Q	T	G	M	G	M	S	T	M	A	R	V	G	S	I	V	S	P	L	V	S	M	T	A	E	480	
Db	421	IIRT	S	L	A	V	L	G	K	G	C	L	A	S	S	F	N	C	I	F	L	Y	T	G	E	L	Y	P	T	V	I	R	Q	T	G	L	G	M	G	S	T	M	A	R	V	G	S	I	V	S	P	L	V	S	M	T	A	E	480
Qy	481	LYPS	M	P	L	F	I	Y	G	A	V	P	V	A	S	A	V	T	V	L	P	E	T	L	G	Q	P	L	P	D	T	V	Q	D	L	E	S	R	W	A	P	T	Q	K	E	A	G	I	Y	P	R	K	G	K	Q	T	540		
Db	481	FYPS	M	P	L	F	I	F	G	A	V	P	V	V	A	S	A	V	T	A	L	P	E	T	L	G	Q	P	L	P	D	T	V	Q	D	L	K	S	R	-----	S	R	G	K	Q	N	528												
Qy	541	RQQE	H	Q	K	Y	M	V	P	L	Q	A	S	A	Q	E	K	N	G	L	563																																						
Db	529	QQQE	Q	Q	K	Q	M	M	P	L	Q	A	S	T	Q	E	K	N	G	L	551																																						

RESULT 6
 Q61185
 ID Q61185 PRELIMINARY; PRT; 545 AA.
 AC Q61185;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE KIDNEY-SPECIFIC TRANSPORT PROTEIN.
 GN SLC22A6.
 OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/C;
 RX MEDLINE=97197822; PubMed=9045672;
 RA Lopez-Nieto C.E., You G., Bush K.T., Barros E.J., Beier D.R.,
 RA Nigam S.K.;
 RT "Molecular cloning and characterization of NKT, a gene product related
 RT to the organic cation transporter family that is almost exclusively
 RT expressed in the kidney."
 RL J. Biol. Chem. 272:6471-6478(1997).
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO THE SUGAR TRANSPORTER FAMILY.
 DR EMBL; U52842; AAC53112.1; -.
 DR MGD; MGI:892001; Slc22a6.
 DR InterPro; IPR003662; sub_transporter.
 DR Pfam; PF00083; sugar_tr; 1.
 KW Transmembrane.
 SQ SEQUENCE 545 AA; 59983 MW; CD3B762E5984933A CRC64;

Query Match 83.5%; Score 2443; DB 11; Length 545;
 Best Local Similarity 83.1%; Pred. No. 1.1e-188;
 Matches 468; Conservative 41; Mismatches 36; Indels 18; Gaps 2;

Qy	1	MAFNDDLQVGGVGRFQQIQVTLVVLPLLLMASHNTLQNFTAAIPTHHCRPPADANLSKN	60
Db	1	MAFNDDLKQVGGVGRFQLIQVTMVVAPLLLMASHNTLQNFTAAIPAHHCRPPANANLSKD	60
Qy	61	GGLEVWLPRDRQQPESCLRFTSPQWGLPFLNGTEANGTGATEPCTDGWIYDNSTFPSTI	120
Db	61	GGLEARLPLDKQGRPESCLRFPPH-----NGTEANGTGATEPCLDGWVYDNSTFPSTI	114
Qy	121	VTEWDLVCSHRALRQLAQSLYMGVLLGAMVFGYLADRLGRRKVLIILNYLQTAVSGTCAA	180
Db	115	VTEWNLVCSHRAFRQLAQSLFMVGVLLGAMMFGYLADRLGRRKVLIILNYLQTAVSGTCAA	174
Qy	181	FAPNFPPIYCAFRLLSGMALAGISLNCMTLNVEWMPHTRACVGTIGYVYSLGQFLLAGV	240
Db	175	YAPNYTVYICIFRLLSGMSLASIAINCMTLNMEWMPHTRAYVGTIGYVYSLGQFLLAGI	234
Qy	241	AYAVPHWRHLQLLVSAPFFAFFIYSWFFIESARWHSSSGLDLTLRALQVARINGKREE	300
Db	235	AYAVPHWRHLQLAVSVPPFFVAFIYSWFFIESARWYSSSGLDLTLRALQVARINGKQEE	294
Qy	301	GAKLSMEVLRASLQKELTMGKGQASAMELLRCPTLRHLFLCLSMWLFATSFAYYGLVMDL	360
Db	295	GAKLSIEVLQTSLQKELTLNKGQASAMELLRCPTLRRLFLCLSMWLFATSFAYYGLVMDL	354
Qy	361	QGFGVSIYLIQVIFGAVDLPKLVGFLVINSIGRRPAQMAALLLAGICILNGVIPQDQS	420
Db	355	QGFGVSMYLIQVIFGAVDLPKLVCFVINSIGRRPAQLASLLLAGICILVNGIIPRGHT	414
Qy	421	IVRTSLAVLGKGCLAA SFNCIFLYTGELYPTMIRQTGMGMGSTMARVGSIVSPLVSMTAE	480
Db	415	IIRTS LAVLGKGCLAA SFNCIFLYTGELYPTMIRQTGLGMGSTMARVGSIVSPLISMTAE	474
Qy	481	LYPSMPLFIYGAVPVAASAVTVLLPETLGQPLPDTVQDLESRWAPTQKEAGIYPRKGKQT	540
Db	475	FYPSIPLFIYGAVPVAASAVTALLPETLGQPLPDTVQDLKSR-----SRGKQK	522
Qy	541	RQQQEHQKYMVPLQASAEKNGL	563
Db	523	QQQLEQQKQMIPLQVSTQEKNGL	545

RESULT 7

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ID 057379          PRELIMINARY;          PRT;      562 AA.
AC 057379;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE RENAL ORGANIC ANION TRANSPORTER.
OS Pseudopleuronectes americanus (Winter flounder).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
OC Pleuronectoidei; Pleuronectidae; Pseudopleuronectes.
OX NCBI_TaxID=8265;
RN [1]
RP SEQUENCE FROM N.A., AND FUNCTION.
RC TISSUE=KIDNEY;
RX MEDLINE=98072393; PubMed=9409735;
RA Wolff N.A., Werner A., Burkhardt S., Burckhardt G.;
RT "Expression cloning and characterization of a renal organic anion
RT transporter from winter flounder.";
RL FEBS Lett. 417:287-291(1997).
CC -!- FUNCTION: MEDIATES THE NA(+)-INDEPENDENT TRANSPORT OF ORGANIC
CC ANIONS SUCH AS P-AMINOHIPPURATE.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. BASOLATERAL
CC MEMBRANE (POTENTIAL).
CC -!- PTM: GLYCOSYLATED (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE SLC21 FAMILY OF TRANSPORTERS.
DR EMBL; Z97028; CAB09724.1; -.
DR InterPro; IPR003662; sub_transporter.
DR Pfam; PF00083; sugar_tr; 1.
KW Transmembrane; Transport; Glycoprotein; Ion transport.
FT TRANSMEM      148      168      POTENTIAL.
FT TRANSMEM      175      195      POTENTIAL.
FT TRANSMEM      206      226      POTENTIAL.
FT TRANSMEM      261      281      POTENTIAL.
FT TRANSMEM      409      429      POTENTIAL.
FT TRANSMEM      496      516      POTENTIAL.
FT CARBOHYD       54       54      N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD       95       95      N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD      124      124      N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE      562 AA;   61992 MW;  7DC1A67F32801D2D CRC64;

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Qy	1	MAFNDDLQQVGVGFRQQIQVTLVLVPLLLMASHNTLQNFTAAIPTHCRPPAD---	ANL	57
Db	1	MPFSELLEQVGSTGRFQVLHVTLCLIPVLLMMASHNLLQNFFVATVP	SHYCNANHANLSQARL	60
Qy	58	SKNGGLEVLWLPDRDQGPESCLRFTSPQWGLPFLNGTEANG-----	TGATEPCTDG	108
Db	61	SLEESLLITVPLDGAQKQRCQRYAAPQWHLLGKNGTSGSGDLADATESMDAALQECS	SDG	120
Qy	109	WIYDNSTFPSTIVTEWDLVCSHRALRQLAQSLYMGVGLGAMVFGYLADRLGRRKVLILN		168
Db	121	WSYNSTVRSSTIISEWHLVCDMHSFKQMGQTIYMGVVLGALLFGGLSDRYGRRILLIS		180
Qy	169	YLQTAVSGTCAAFAPNFPIYCAFRLLSGMALAGISLNCMTLNVEWMPHTRACVGT	LIGY	228
Db	181	NLLMAVSGTCAAFSSSFLFCVFRFGCGLALSGGLGLNTFSLIVEWIPTRIRTA	VGTGTTGY	240
Qy	229	VYSLGQFLLAGVAYAVPHWRHLQLLVSAFFFAFFIYSWFFIESARWHSSSGRLDL	TLRAL	288
Db	241	CYTLGQLILVLLAYFIRDWRWLTAVSLPFIYVFFLIAWWFHESSRWLALSNRTE	HALKNL	300
Qy	289	QRVARINGKREEGAKLSMEVLRASLQKELTMGKGQASAMELLRCPTLRHLFLC	LSMLWFA	348
Db	301	KSVARFNGRHEEAELDKIMLHESMKKEMSCOTGSYSILDFTNPAMRKRTLCLSA	VAWL	360

Qy 349 TSFAYYGLVMDLQGFVSIYLIQVIFGAVDLPKLVGFLVINSIGRRPAQMAALLLAGIC 408
 ||||| ||| ||| ||||| ||||| ||||| : : : ||| : | |||||
 Db 361 TSFAYYGLAMDLDKFGVDIYLIQVIFGAVDIPAKVVVVVMSLIGRRRSQCAVLVVAGIT 420
 Qy 409 ILLNGVIPQDQSIVRTSLAVLGKGCCLAASFNCIFLYTGELYPTMIRQTGMGMGSTMARVG 468
 |||| : : | : ||| ||||| ||||| ||||| : ||| : ||| : ||| ||| | ||| : |
 Db 421 ILLNLLVPYDKQTIRTCLAVLGKGCCLAASFNCYLYSGELFPTIIRQNGMGWVSMMARIG 480
 Qy 469 SIVSPLVSMTAELYPSPMLFIYGAVPVAASAVTVLLPETLGQPLPDTVQDLESRWAPTQK 528
 : : : : | : | : | ||| : : : ||||| ||||| : ||| :
 Db 481 AMVAPMVLTRDYIPWLPGLIYGGAPILSGLAAIFLPETLGYPPLDTIQDVE----- 532
 Qy 529 EAGIYPRKGKQTRQQ 543
 | : | || | : : :
 Db 533 ESG-SGRKSKMSTKE 546

RESULT 12

OS4778

ID OS4778 PRELIMINARY; PRT; 553 AA.
 AC OS4778;
 DT 01-JUN-1998 (TrEMBLrel. 06, Created)
 DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE RST.
 GN SLC22A2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=KIDNEY;
 RX MEDLINE=98072412; PubMed=9409754;
 RA Mori K., Ogawa Y., Ebihara K., Aoki T., Tamura N., Sugawara A.,
 RA Kuwahara T., Ozaki S., Mukoyama M., Tashiro K., Tanaka I., Nakao K.;
 RT "Kidney-specific expression of a novel mouse organic cation
 RT transporter-like protein.";
 RL FEBS Lett. 417:371-374(1997).
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO THE SUGAR TRANSPORTER FAMILY.
 DR EMBL; AB005451; BAA23875.1; -.
 DR MGD; MGI:1195269; Slc22a2.
 DR InterPro; IPR003662; sub_transporter.
 DR Pfam; PF00083; sugar_tr; 1.
 KW Transmembrane.
 SQ SEQUENCE 553 AA; 60160 MW; D991F5F74A39BBBF CRC64;

Query Match 43.3%; Score 1267.5; DB 11; Length 553;
 Best Local Similarity 46.9%; Pred. No. 6.5e-94;
 Matches 250; Conservative 91; Mismatches 181; Indels 11; Gaps 3;

Qy 1 MAFNDLLQQVGVGRFQQIQVTLVVLPLLLMASHNTLQNFTAAIPTHCRPP-----AD 54
 ||| : || : ||| : ||| | : | : | : | : ||| : ||| :
 Db 1 MAFPELLDRVGGGLGRFQLFQTVALVTPILWVTTQNMLENFSAAVPHHRCWVPLLDNSTSQ 60
 Qy 55 ANLSKNGG----LEVWLPRDRQGQPECLRFTSPQWGLPPLNGTEAN-GTGATEPCTDGW 109
 | : : | | : | ||| ||| | | | ||||| |||
 Db 61 ASIPGDLGPDVLLAVSIPPGPDQQPHQCLFRFPQWQLTESNATATNWSDAATEPCEDGW 120
 Qy 110 IYDNSTFPSTIVTEWDLVCSHRALRQLAQSLYMGVLLGAMVFGYLADRLGRRKVLILNY 169
 : ||| ||| ||||| : ||| : ||| : : | : | : | ||| : |
 Db 121 VYDHSFTRSTIVTTWDLVCNSQALRPMAQSIFLAGILVGAACVGHASDRFGRRLVLTWSY 180
 Qy 170 LQTAVSGTCAAFAPNFPIYCAFRLLSGMALAGISLNCMTLNVEWMPHTRACVGTIGYV 229
 | : ||| ||| | ||| || | : ||| : | : | : ||
 Db 181 LLVSVSGTAAAFMPTFFPLYCLFRFLASAVAGVMMNTASLLMEWTSAQGSPLVMTLNALG 240
 Qy 230 YSLGQFLLAGVAYAVPHWRHLQLLVSAPFFAFFIYSWFFIESARWHSSSRLDLTLRALQ 289

Db	241	FSFGQVLTSVAYGVRSWRMLQLAVSAPFFLFFVYSWWLPESARWLITVVGKLDQGLQELQ	300
Qy	290	RVARINGKREEGAKLSMEVLRASLQKELTMGKGQASAMELLRCPTLRHLFLCLSMLWFAT	349
Db	301	RVAAVNRRKAEGDTLTMEVLRSAMEEPEPSRDKAGASLGTLLHTPGLRHRTIISMLCWFAF	360
Qy	350	SFAYYGLVMDLQGFVGSYIYLIQVIFGAVDLPKLVGFLVINSLGRPPAQMAALLLAGICI	409
Db	361	GFTFYGLALDLQALGSNIFLLQALIGIVDFPVKTSGLLISRLGRRLCQVSFLVLPGLCI	420
Qy	410	LLNGVIPQDQSIVRTSLAVLGKGCLAA SFNCIFLYTGELYPTMIRQTGMGMGSTMARVGS	469
Db	421	LSNILVPHGMGVLRSALAVLGLGCLGGAFTCITIFSELFPVTIRM TAVGLCQVAARGGA	480
Qy	470	IVSPLVSMTAEYLPSPMLFIYGAVPVAASAVTVLLPETLGQPLPDTVQDLESR	522
Db	481	MLGPLVRLGLGVYGSWMLLVYGVVPVLSGLAALLPETKNPLPDTIQDIQKQ	533